

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> Aspartate Kinase

<130> BB1430 PCT

<140>

<141>

<150> 60/172944

<151> 1999-12-21

<160> 24

<170> Microsoft Office 97

<210> 1

<211> 565

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (127)

<400> 1

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ctttgaagac gatgtcctat cacaagtcga agcggagaac ctactcgtgg gctgatcaac 300
gtaggctttg ctgggtccag gcgtgttatc tgttatagat tcccactcgc ctccatgaac 360
ggcatgggca ttggatcatt gatcatgttt tgcttgaaac aagtatgtct tccaggttct 420
cagccaatga ctgcaaaact gtgtttctgt tttagaactg tttgcagaca ccagtgaact 480
gcgagcaccg attgtcaaca agatggcaag cctgtgatat aattccaact gtctctaact 540
aatatatata ataaacatta tcaat                                     565

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<210> 2

<211> 97

<212> PRT

<213> Zea mays

<220>

<221> UNSURE

<222> (42)

<400> 2

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Gln Arg Ala Ile Ile Ser Leu Ile Gly Asn Val Glu Gln Ser Ser Leu
          20             25             30

Ile Leu Glu Lys Thr Gly Arg Val Leu Xaa Glu Ser Gly Val Asn Val
  35             40             45

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Gln Met Ile Ser Gln Gly Ala Ser Lys Val Asn Met Ser Leu Ile Val  
 50 55 60

His Asp Ser Asp Ala Lys Ala Leu Val Glu Ala Leu His Gln Ala Phe  
 65 70 75 80

Phe Glu Asp Asp Val Leu Ser Gln Val Glu Ala Glu Asn Leu Leu Val  
 85 90 95

Gly

<210> 3  
 <211> 513  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (474)

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 acccgaaccg ggcctcgcgg tgcaagaggg ttgtcaatgg tggtcgccga ctccaccagc 180  
 cgtcggggcca agcaagcggg cggcggggac ggcgtccttg gggcgccctgt tctcggaggg 240  
 ctcggggatgg agggattggg ggatcagctc agcgttggtga tgaagttcgg ggggtcctcg 300  
 gtgtcgtcgg ccgcgaggat ggctgaggtg gccggcctca tcctgacgtt ccccgaggag 360  
 cgccccgctg tcgttctctc tgccatgggg aaaaccacca acaaccttct ccttgctggg 420  
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 tcaaaaagcc taaaatatca aagtatccca act 513

<210> 4  
 <211> 152  
 <212> PRT  
 <213> Zea mays

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Ala Pro Arg Arg Leu Val Pro Ser Ile Pro Pro Ala Ser Ser Gly His  
 20 25 30

Val Arg Gly Leu Ala Cys Phe Gly Thr Arg Thr Gly Pro Arg Gly Ala  
 35 40 45

Arg Gly Leu Ser Met Val Val Ala Asp Ser Thr Ser Arg Arg Ala Lys  
 50 55 60

Gln Ala Asp Gly Gly Asp Gly Val Leu Gly Ala Pro Val Leu Gly Gly  
 65 70 75 80

Leu Gly Met Glu Gly Leu Gly Asp Gln Leu Ser Val Val Met Lys Phe  
 85 90 95

Gly Gly Ser Ser Val Ser Ser Ala Ala Arg Met Ala Glu Val Ala Gly  
 100 105 110

Leu Ile Leu Thr Phe Pro Glu Glu Arg Pro Val Val Val Leu Ser Ala  
 115 120 125

Met Gly Lys Thr Thr Asn Asn Leu Leu Leu Ala Gly Arg Lys Gly Asn  
 130 135 140

Lys Val Trp Ser Tyr His Val Phe  
 145 150

<210> 5  
 <211> 1985  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (532)

<220>  
 <221> unsure  
 <222> (1180)

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 caccagccgt cgggccaagc aagcggacgg cggggacggc gtccttgggg cgcctgttct 240  
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 gtccctcggtg tcgtcggccg cgaggatggc tgagggtggc gccctcatcc tgacgttccc 360  
 cgaggagcgc ccgcgtcgctg ttctctctgc catggggaaa accaccaaca accttctcct 420  
 tgctggagag aaggcagtag ggtgtggagt tatccatgtt tctgaaatcg aagagtggaa 480  
 tatggtcaaa agcctacata tcaagacggg ggatgaactt ggacttccaa gnatctgtaa 540  
 tacaagcctt tatgaactgg agcaactatt gaaaggtatc gctatgatga aagagctgac 600  
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 atttgaagag gccacagaac ttgcttattt tgggtgctcag gttttgcac cacaatcgat 1080  
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 tccaggcacc cttattacca gacaaagaga catggataa ggtctggttg tactaactag 1200  
 catagtgtc aagtcaaag tcaactatgtt ggacattgtg agcactcgga tgcttgggtca 1260  
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 atgttttgct tgaacaagt atgtcttcca ggttctcagc caatgactgc aaaactgtgt 1860  
 ttctgtttta gaactgtttg cagacaccag tgagctgcga gcaccgattg tcaacaagat 1920  
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<210> 6  
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 <212> PRT  
 <213> Zea mays

<220>  
 <221> UNSURE  
 <222> (168)

<220>  
 <221> UNSURE  
 <222> (384)

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             20                    25                    30  
 Gly Thr Arg Thr Gly Pro Arg Gly Ala Arg Gly Leu Ser Met Val Val  
             35                    40                    45  
 Ala Asp Ser Thr Ser Arg Arg Ala Lys Gln Ala Asp Gly Gly Asp Gly  
             50                    55                    60  
 Val Leu Gly Ala Pro Val Leu Gly Gly Leu Gly Met Glu Gly Leu Gly  
             65                    70                    75                    80  
 Asp Gln Leu Ser Val Val Met Lys Phe Gly Gly Ser Ser Val Ser Ser  
             85                    90                    95  
 Ala Ala Arg Met Ala Glu Val Ala Gly Leu Ile Leu Thr Phe Pro Glu  
             100                    105                    110  
 Glu Arg Pro Val Val Val Leu Ser Ala Met Gly Lys Thr Thr Asn Asn  
             115                    120                    125  
 Leu Leu Leu Ala Gly Glu Lys Ala Val Gly Cys Gly Val Ile His Val  
             130                    135                    140  
 Ser Glu Ile Glu Glu Trp Asn Met Val Lys Ser Leu His Ile Lys Thr  
             145                    150                    155                    160  
 Val Asp Glu Leu Gly Leu Pro Xaa Ile Cys Asn Thr Ser Leu Tyr Glu  
             165                    170                    175  
 Leu Glu Gln Leu Leu Lys Gly Ile Ala Met Met Lys Glu Leu Thr Pro  
             180                    185                    190  
 Arg Thr Ser Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser Thr Arg  
             195                    200                    205  
 Ile Phe Ser Ala Tyr Leu Asn Lys Ile Arg Val Lys Ala Arg Gln Tyr  
             210                    215                    220  
 Asp Ala Phe Asp Ile Gly Phe Ile Thr Thr Asp Glu Phe Gly Asn Ala  
             225                    230                    235                    240

Asp Ile Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu His Gly  
 245 250 255  
 Asp Trp Ile Gln Asp Pro Ala Ile Pro Val Val Thr Gly Phe Leu Gly  
 260 265 270  
 Lys Gly Trp Lys Ser Gly Ala Val Thr Thr Leu Gly Arg Gly Gly Ser  
 275 280 285  
 Asp Leu Thr Ala Thr Thr Ile Gly Lys Ala Leu Gly Leu Arg Glu Ile  
 290 295 300  
 Gln Val Trp Lys Asp Val Asp Gly Val Leu Thr Cys Asp Pro Asn Ile  
 305 310 315 320  
 Tyr Pro His Ala Lys Thr Val Pro Tyr Leu Thr Phe Glu Glu Ala Thr  
 325 330 335  
 Glu Leu Ala Tyr Phe Gly Ala Gln Val Leu His Pro Gln Ser Met Arg  
 340 345 350  
 Pro Ala Arg Glu Gly Asp Ile Pro Val Arg Val Lys Asn Ser Tyr Asn  
 355 360 365  
 Pro Lys Ala Pro Gly Thr Leu Ile Thr Arg Gln Arg Asp Met Asp Xaa  
 370 375 380  
 Gly Leu Val Val Leu Thr Ser Ile Val Leu Lys Ser Asn Val Thr Met  
 385 390 395 400  
 Leu Asp Ile Val Ser Thr Arg Met Leu Gly Gln Tyr Gly Phe Leu Ala  
 405 410 415  
 Arg Val Ser Gly Ile Cys Tyr Ile Glu Asp Leu Cys Ile Ser Val Asp  
 420 425 430  
 Cys Val Ala Thr Ser Glu Val Ser Val Ser Val Ser Leu Asp Pro Ser  
 435 440 445  
 Lys Ile Trp Ser Arg Glu Leu Ile Gln Gln Ala Ser Glu Leu Asp His  
 450 455 460  
 Val Val Glu Glu Leu Glu Lys Ile Ala Ile Val Arg Leu Leu Gln Gln  
 465 470 475 480  
 Arg Ala Ile Ile Ser Leu Ile Gly Asn Val Glu Gln Ser Ser Leu Ile  
 485 490 495  
 Leu Glu Lys Thr Gly Arg Val Leu Arg Lys Ser Gly Val Asn Val Gln  
 500 505 510  
 Met Ile Ser Gln Gly Ala Ser Lys Val Asn Met Ser Leu Ile Val His  
 515 520 525  
 Asp Ser Asp Ala Lys Ala Leu Val Glu Ala Leu His Gln Ala Phe Phe  
 530 535 540  
 Glu Asp Asp Val Leu Ser Gln Val Glu Ala Glu Asn Leu Leu Val Gly  
 545 550 555 560

<210> 7  
 <211> 1953  
 <212> DNA  
 <213> Zea mays

<400> 7  
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 cgaaccgggc ctccggtgac aagaggggttg tcaatgggtg tcgccgactc caccagccgt 180  
 cgggccaaag aagcggacgg cggggacggc gtccctgggg cgccctgttct cggagggctc 240  
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 accattggta aagccttggg actgagagaa attcaggtat ggaaagatgt tgatggtgta 960  
 cttacttgtg atccaaatat ctaccacat gcaaagactg ttccatactt aacatttgaa 1020  
 gaggccacag aacttgccta ttttgggtgt caggttttgc atccacaatc gatgagacct 1080  
 gctagagaag gtgatattcc agttagggtt aagaattcat acaaccctaa agctccaggc 1140  
 accttatta ccagacaaag agacatggat aaggttgtac taactagcat agtgctcaag 1200  
 tcaaagtgtc ctatgttgga cattgtgagc actcggatgc ttggtcagta tggttttctg 1260  
 gcaaggggtat ttgctatatt tgaagatcta tgtatatctg tggattgtgt tgctaccagt 1320  
 gaagttagtg tttctgtgtc acttgatcca tcaaagatct ggagtaggga actgatacag 1380  
 caggaacttg accatgtagt tgaagagctt gagaaaatag caattgttcg tctacttcag 1440  
 cagagggcga taatttcact tatcggaaat gtggagcaat cgtctctcat actagaaaag 1500  
 acgggacgtg tgctgaggaa aagtgggtt aatgttcaga tgatctcgca aggagcgtca 1560  
 aaggttaaca tgtcgtgat agtccatgat agcgatgcaa aggcactcgt agaagccctt 1620  
 catcaggcgt tctttgaaga cgatgtccta tcacaagtcg aagcggagaa cctactcgtg 1680  
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 cctccatgaa cggcatgggc attggatcat tgatcatgtt ttgcttgaaa caagtatgtc 1800  
 ttccagggtt tcagccaatg actgcaaaac tgtgtttctg ttttagaact gtttgagac 1860  
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 tgtctctaata caatatatat aataaacatt atc 1953

<210> 8  
 <211> 555  
 <212> PRT  
 <213> Zea mays

<400> 8  
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 20 25 30  
 Gly Thr Arg Thr Gly Pro Arg Gly Ala Arg Gly Leu Ser Met Val Val  
 35 40 45  
 Ala Asp Ser Thr Ser Arg Arg Ala Lys Gln Ala Asp Gly Gly Asp Gly  
 50 55 60

Val Leu Gly Ala Pro Val Leu Gly Gly Leu Gly Met Glu Gly Leu Gly  
 65 70 75 80  
 Asp Gln Leu Ser Val Val Met Lys Phe Gly Gly Ser Ser Val Ser Ser  
 85 90 95  
 Ala Ala Arg Met Ala Glu Val Ala Gly Leu Ile Leu Thr Phe Pro Glu  
 100 105 110  
 Glu Arg Pro Val Val Val Leu Ser Ala Met Gly Lys Thr Thr Asn Asn  
 115 120 125  
 Leu Leu Leu Ala Gly Glu Lys Ala Val Gly Cys Gly Val Ile His Val  
 130 135 140  
 Ser Glu Ile Glu Glu Trp Asn Met Val Lys Ser Leu His Ile Lys Thr  
 145 150 155 160  
 Val Asp Glu Leu Gly Leu Pro Arg Ser Val Ile Gln Asp Met Leu Asp  
 165 170 175  
 Glu Leu Glu Gln Leu Leu Lys Gly Ile Ala Met Met Lys Glu Leu Thr  
 180 185 190  
 Pro Arg Thr Ser Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser Thr  
 195 200 205  
 Arg Ile Phe Ser Ala Tyr Leu Asn Lys Ile Arg Val Lys Ala Arg Gln  
 210 215 220  
 Tyr Asp Ala Phe Asp Ile Gly Phe Ile Thr Thr Asp Glu Phe Gly Asn  
 225 230 235 240  
 Ala Asp Ile Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu His  
 245 250 255  
 Gly Asp Trp Ile Gln Asp Pro Ala Ile Pro Val Val Thr Gly Phe Leu  
 260 265 270  
 Gly Lys Gly Trp Lys Ser Gly Ala Val Thr Thr Leu Gly Arg Gly Gly  
 275 280 285  
 Ser Asp Leu Thr Ala Thr Thr Ile Gly Lys Ala Leu Gly Leu Arg Glu  
 290 295 300  
 Ile Gln Val Trp Lys Asp Val Asp Gly Val Leu Thr Cys Asp Pro Asn  
 305 310 315 320  
 Ile Tyr Pro His Ala Lys Thr Val Pro Tyr Leu Thr Phe Glu Glu Ala  
 325 330 335  
 Thr Glu Leu Ala Tyr Phe Gly Ala Gln Val Leu His Pro Gln Ser Met  
 340 345 350  
 Arg Pro Ala Arg Glu Gly Asp Ile Pro Val Arg Val Lys Asn Ser Tyr  
 355 360 365  
 Asn Pro Lys Ala Pro Gly Thr Leu Ile Thr Arg Gln Arg Asp Met Asp  
 370 375 380

Lys Val Val Leu Thr Ser Ile Val Leu Lys Ser Asn Val Thr Met Leu  
 385 390 395 400  
 Asp Ile Val Ser Thr Arg Met Leu Gly Gln Tyr Gly Phe Leu Ala Arg  
 405 410 415  
 Val Phe Ala Ile Phe Glu Asp Leu Cys Ile Ser Val Asp Cys Val Ala  
 420 425 430  
 Thr Ser Glu Val Ser Val Ser Val Ser Leu Asp Pro Ser Lys Ile Trp  
 435 440 445  
 Ser Arg Glu Leu Ile Gln Gln Glu Leu Asp His Val Val Glu Glu Leu  
 450 455 460  
 Glu Lys Ile Ala Ile Val Arg Leu Leu Gln Gln Arg Ala Ile Ile Ser  
 465 470 475 480  
 Leu Ile Gly Asn Val Glu Gln Ser Ser Leu Ile Leu Glu Lys Thr Gly  
 485 490 495  
 Arg Val Leu Arg Lys Ser Gly Val Asn Val Gln Met Ile Ser Gln Gly  
 500 505 510  
 Ala Ser Lys Val Asn Met Ser Leu Ile Val His Asp Ser Asp Ala Lys  
 515 520 525  
 Ala Leu Val Glu Ala Leu His Gln Ala Phe Phe Glu Asp Asp Val Leu  
 530 535 540  
 Ser Gln Val Glu Ala Glu Asn Leu Leu Val Gly  
 545 550 555

<210> 9  
 <211> 455  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> unsure  
 <222> (366)

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aatccaatca	ccctgtaacc	tctttgcaac	agcaggatat	gtcgcttcaa	gaatgtccgc		180
atttgtgaaa	tcatcagtag	ttataaagcc	aatatcaaat	gcatacatact	gccgagcctt		240
tttcccaagt	ttattcaaat	atgcaagcaa	atattcttgt	agacatgc	at	taccgaagg	300
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aagaangttg	gttccaattc	cttccaataa	aaanccttga	aacaantccg	gatnctaatac		420
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<210> 10
<211> 114
<212> PRT
<213> Oryza sativa
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<400> 10
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Val Asn Ala Cys Leu Gln Glu Tyr Leu Leu Ala Tyr Leu Asn Lys Leu
          20          25          30
Gly Lys Lys Ala Arg Gln Tyr Asp Ala Phe Asp Ile Gly Phe Ile Thr
          35          40          45
Thr Asp Asp Phe Thr Asn Ala Asp Ile Leu Glu Ala Thr Tyr Pro Ala
          50          55          60
Val Ala Lys Arg Leu Gln Gly Asp Trp Ile Asp Asp Pro Ala Ile Pro
          65          70          75          80
Ile Val Thr Gly Phe Leu Gly Lys Gly Trp Lys Ser Cys Ala Val Thr
          85          90          95
Thr Leu Gly Arg Gly Gly Ser Asp Leu Thr Ala Thr Thr Ile Gly Lys
          100          105          110
Ala Leu

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<210> 11
<211> 847
<212> DNA
<213> Oryza sativa
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ttgtctctcaa	caaggacgac	gcggcgctcg	tgccgcgcgc	cgccgcctcc	tccgcgacgg				180
ggttcaccgt	gcccatgaaq	ttcggcgggt	cgctcggtg	gtcggcggaq	cggatgcggg				240

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aggtggccga tctcatactc agcttccccg aggagactcc cgttggtggt ctctccgcca 300
tggggaagac caccaataac ctctcctcgg ccggagagaa ggctgtcagc tgcggcgccc 360
cgaaggcgtc tgaaattccc gagctcgcag ttatcaagga gctccatgtt aggactattg 420
atgagcttgg attggataga tcgattgttt cagggtttatt ggaagaattg gaacaacttc 480
ttaagggtgt tgctatgatg aaagaactaa ctctaggac acgggattac cttgtttcct 540
tcggtgaatg catgtctaca agaatatatt ctgcatattt gaataaactt gggaaaaagg 600
ctcggcagta tgatgcattt gatattggct ttataactac tgatgatttc acaaatgcgg 660
acattcttga agcgacatat cctgctgttg caaagagggt acagggtgat tggattgacg 720
accctgctat tcctatagtt actggtttcc ttggaaaagg atggaaatca tgtgctgtca 780
ccactttagg cagagggtggc agcgacttga ctgctaccac cattggcaaa gcgttgcgga 840
cgcggtgg                                     847

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&lt;210&gt; 12

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Oryza sativa

&lt;400&gt; 12

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Pro Pro Arg Val Gly Arg Glu Gln Gln Tyr Leu Ala Cys Ala Ala Ala
  1              5              10              15

Ala Arg Pro Gly Gly Arg Cys Ser Arg Arg Arg Gly Leu Val Val Arg
          20              25              30

Cys Gln Ser Gly Ala Ala Ala Val Val Leu Asn Lys Asp Asp Ala Ala
          35              40              45

Ser Val Ala Ala Ala Ala Ala Ser Ser Ala Thr Gly Phe Thr Val Ala
          50              55              60

Met Lys Phe Gly Gly Ser Ser Val Ala Ser Ala Glu Arg Met Arg Glu
          65              70              75              80

Val Ala Asp Leu Ile Leu Ser Phe Pro Glu Glu Thr Pro Val Val Val
          85              90              95

Leu Ser Ala Met Gly Lys Thr Thr Asn Asn Leu Leu Leu Ala Gly Glu
          100             105             110

Lys Ala Val Ser Cys Gly Ala Pro Lys Ala Ser Glu Ile Pro Glu Leu
          115             120             125

Ala Val Ile Lys Glu Leu His Val Arg Thr Ile Asp Glu Leu Gly Leu
          130             135             140

Asp Arg Ser Ile Val Ser Gly Leu Leu Glu Glu Leu Glu Gln Leu Leu
          145             150             155             160

Lys Gly Val Ala Met Met Lys Glu Leu Thr Pro Arg Thr Arg Asp Tyr
          165             170             175

Leu Val Ser Phe Gly Glu Cys Met Ser Thr Arg Ile Phe Ala Ala Tyr
          180             185             190

Leu Asn Lys Leu Gly Lys Lys Ala Arg Gln Tyr Asp Ala Phe Asp Ile
          195             200             205

Gly Phe Ile Thr Thr Asp Asp Phe Thr Asn Ala Asp Ile Leu Glu Ala
          210             215             220

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Thr Tyr Pro Ala Val Ala Lys Arg Leu Gln Gly Asp Trp Ile Asp Asp  
 225 230 235 240  
 Pro Ala Ile Pro Ile Val Thr Gly Phe Leu Gly Lys Gly Trp Lys Ser  
 245 250 255  
 Cys Ala Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Leu Thr Ala Thr  
 260 265 270  
 Thr Ile Gly Lys Ala Leu Arg Thr Arg  
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<210> 13  
 <211> 646  
 <212> DNA  
 <213> Triticum aestivum

<220>  
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&lt;221&gt; unsure

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&lt;400&gt; 13

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cctgggggta agaaaatcag gttggaagat gtaacggttt tgactgtgat caatattatc 540
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&lt;210&gt; 14

&lt;211&gt; 146

&lt;212&gt; PRT

&lt;213&gt; Triticum aestivum

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (110)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (131)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (145)

&lt;400&gt; 14

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Ala Val Ser Cys Gly Ala Pro Lys Ala Ser Glu Ile Tyr Glu Leu Ala
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Val Ile Lys Glu Leu His Leu Arg Thr Ile Asp Glu Leu Gly Leu Asp
          20             25             30
Ser Ser Ile Val Ser Gly Phe Leu Asp Glu Leu Glu Gln Leu Leu Lys
          35             40             45
Gly Val Ala Met Met Lys Glu Leu Thr Leu Arg Thr Arg Asp Tyr Leu
          50             55             60
Val Ser Phe Gly Glu Cys Met Ser Thr Arg Ile Phe Ser Ala Tyr Leu
          65             70             75             80
Asn Lys Leu Gly Lys Lys Ala Arg Gln Tyr Asp Ala Phe Asp Leu Gly
          85             90             95
Phe Ile Thr Thr Gly Arg Phe Pro Gln Met Pro Ile Ser Xaa Asn Asn
          100            105            110
Leu Ser Cys Cys Cys Lys Glu Leu His Gly Asn Trp Leu Met Thr Leu
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Xaa Thr  
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tcagggtttt tggacgagtt ggagcaactg ctcaagggtg ttgctatgat gaaagagctg 180  
actcttagga caccgagatta ccttggttcc tttggtgaat gcatgtctac aagaatattt 240  
tctgcataatt tgaataaact aggaagaag gcacgacagt atgatgcttt tgatcttggc 300  
tttataacca ctgacgattt cacaatgcc gatattctcg aagcaactta tcctgctgtt 360  
gcaaagaggg tacatggaga ttggattgat gaccctgcta ttcctatagt gactggtttc 420  
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accgctacaa ccattggcaa agccttgggg ttaagagaaa ttcagggttg gaaggatgta 540  
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tgtatgtgat tgtgaggcgt cctacttgct gaacttaacc attgtgagga gccctatga 1560  
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1658

<210> 16  
<211> 439  
<212> PRT  
<213> Triticum aestivum

<400> 16  
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Leu Gly Leu Asp Ser Ser Ile Val Ser Gly Phe Leu Asp Glu Leu Glu  
35 40 45  
Gln Leu Leu Lys Gly Val Ala Met Met Lys Glu Leu Thr Leu Arg Thr  
50 55 60

Arg Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser Thr Arg Ile Phe  
 65 70 75 80  
 Ser Ala Tyr Leu Asn Lys Leu Gly Lys Lys Ala Arg Gln Tyr Asp Ala  
 85 90 95  
 Phe Asp Leu Gly Phe Ile Thr Thr Asp Asp Phe Thr Asn Ala Asp Ile  
 100 105 110  
 Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu His Gly Asp Trp  
 115 120 125  
 Ile Asp Asp Pro Ala Ile Pro Ile Val Thr Gly Phe Leu Gly Lys Gly  
 130 135 140  
 Trp Lys Ser Cys Ala Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Leu  
 145 150 155 160  
 Thr Ala Thr Thr Ile Gly Lys Ala Leu Gly Leu Arg Glu Ile Gln Val  
 165 170 175  
 Trp Lys Asp Val Asp Gly Val Leu Thr Cys Asp Pro Asn Ile Tyr Ala  
 180 185 190  
 Asn Ala Val Pro Val Pro Tyr Leu Thr Phe Asp Glu Ala Ala Glu Leu  
 195 200 205  
 Ala Tyr Phe Gly Ala Gln Val Leu His Pro Gln Ser Met Arg Pro Ala  
 210 215 220  
 Arg Glu Gly Gly Ile Pro Val Arg Val Lys Asn Ser Tyr Asn Arg His  
 225 230 235 240  
 Ala Pro Gly Thr Val Ile Thr Lys Thr Arg Asp Met Arg Lys Ser Ile  
 245 250 255  
 Leu Thr Ser Ile Val Leu Lys Ser Asn Ile Thr Met Leu Asp Ile Val  
 260 265 270  
 Ser Thr Arg Met Leu Gly Gln Tyr Gly Phe Leu Ala Lys Val Phe Ser  
 275 280 285  
 Ile Phe Glu Asp Leu Gly Ile Ser Val Asp Ser Val Ala Thr Ser Glu  
 290 295 300  
 Val Ser Ile Ser Leu Thr Leu Asp Pro Ser Lys Leu Trp Ser Arg Glu  
 305 310 315 320  
 Leu Ile Gln Gln Glu Leu Asp His Val Val Glu Glu Leu Glu Lys Ile  
 325 330 335  
 Ala Val Val His Leu Leu Gln His Arg Ser Ile Ile Ser Leu Ile Gly  
 340 345 350  
 Asn Val Gln Arg Ser Ser Leu Ile Leu Glu Lys Ala Phe Asn Val Leu  
 355 360 365  
 Arg Arg Asn Gly Val Asn Val Gln Met Ile Ser Gln Gly Ala Ser Lys  
 370 375 380

Val Asn Ile Ser Leu Val Val Asn Asp Ser Glu Ala Lys Gln Cys Val  
 385 390 395 400

Gln Ala Leu His Ser Ala Phe Phe Glu Asn Gly Phe Leu Ser Glu Val  
 405 410 415

Glu Glu Ala Asp Leu Ala Gln Lys Arg Ala Pro Val Leu Val Ser Ser  
 420 425 430

Asn Gly Ala Ile Asn Gly Asn  
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<210> 17  
 <211> 564  
 <212> PRT  
 <213> Glycine max

<400> 17  
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Gly Phe Ala Ala Leu Gly Ala Pro Val Cys Ala Arg Arg Val Trp Gly  
 35 40 45

Asn Arg Val Ala Phe Ser Val Thr Thr Cys Lys Ala Ser Thr Ser Asp  
 50 55 60

Val Ile Glu Lys Asn Ala Thr Glu Asn Gly Met Val Ser Ser Glu Gly  
 65 70 75 80

Glu Thr Ser Phe Thr Cys Val Met Lys Phe Gly Gly Ser Ser Val Ala  
 85 90 95

Ser Ala Asp Arg Met Lys Glu Val Ala Thr Leu Ile Leu Ser Phe Pro  
 100 105 110

Glu Glu Arg Pro Ile Val Val Leu Ser Ala Met Gly Lys Thr Thr Asn  
 115 120 125

Lys Leu Leu Leu Ala Gly Glu Lys Ala Val Ser Cys Gly Val Ile Asn  
 130 135 140

Val Ser Ser Ile Glu Glu Leu Cys Phe Ile Lys Asp Leu His Leu Arg  
 145 150 155 160

Thr Val Asp Gln Leu Gly Val Asp Gly Ser Val Ile Ser Lys His Leu  
 165 170 175

Glu Glu Leu Glu Gln Leu Leu Lys Gly Ile Ala Met Met Lys Glu Leu  
 180 185 190

Thr Lys Arg Thr Gln Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser  
 195 200 205

Thr Arg Ile Phe Ala Ala Tyr Leu Asn Lys Ile Gly Val Lys Ala Arg  
 210 215 220  
 Gln Tyr Asp Ala Phe Glu Ile Gly Phe Ile Thr Thr Asp Asp Phe Thr  
 225 230 235 240  
 Asn Ala Asp Ile Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu  
 245 250 255  
 His Gly Asp Trp Leu Ser Asp Pro Ala Ile Ala Ile Val Thr Gly Phe  
 260 265 270  
 Leu Gly Lys Ala Arg Lys Ser Cys Ala Val Thr Thr Leu Gly Arg Gly  
 275 280 285  
 Gly Ser Asp Leu Thr Ala Thr Thr Ile Gly Lys Ala Leu Gly Leu Pro  
 290 295 300  
 Glu Ile Gln Val Trp Lys Asp Val Asp Gly Val Leu Thr Cys Asp Pro  
 305 310 315 320  
 Asn Ile Tyr Pro Lys Ala Glu Pro Val Pro Tyr Leu Thr Phe Asp Glu  
 325 330 335  
 Ala Ala Glu Leu Ala Tyr Phe Gly Ala Gln Val Leu His Pro Gln Ser  
 340 345 350  
 Met Arg Pro Ala Arg Glu Ser Asp Ile Pro Val Arg Val Lys Asn Ser  
 355 360 365  
 Tyr Asn Pro Lys Ala Pro Gly Thr Leu Ile Thr Lys Ala Arg Asp Met  
 370 375 380  
 Ser Lys Ala Val Leu Thr Ser Ile Val Leu Lys Arg Asn Val Thr Met  
 385 390 395 400  
 Leu Asp Ile Ala Ser Thr Arg Met Leu Gly Gln Tyr Gly Phe Leu Ala  
 405 410 415  
 Lys Val Phe Ser Ile Phe Glu Glu Leu Gly Ile Ser Val Asp Val Val  
 420 425 430  
 Ala Thr Ser Glu Val Ser Val Ser Leu Thr Leu Asp Pro Ser Lys Leu  
 435 440 445  
 Trp Ser Arg Glu Leu Ile Gln Gln Ala Ser Glu Leu Asp His Val Val  
 450 455 460  
 Glu Glu Leu Glu Lys Ile Ala Val Val Asn Leu Leu Gln Asn Arg Ser  
 465 470 475 480  
 Ile Ile Ser Leu Ile Gly Asn Val Gln Arg Ser Ser Leu Ile Leu Glu  
 485 490 495  
 Arg Leu Ser Arg Val Leu Arg Thr Leu Gly Val Thr Val Gln Met Ile  
 500 505 510  
 Ser Gln Gly Ala Ser Lys Val Asn Ile Ser Leu Val Val Asn Asp Ser  
 515 520 525



Glu Ala Glu Gln Cys Val Arg Ala Leu His Ser Ala Phe Phe Glu Ser  
 530 535 540

Glu Leu Ser Glu Leu Glu Met Asp Tyr Lys Asn Gly Asn Gly Ser Val  
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Asp Glu Leu Ser

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<220>  
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<400> 18  
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<210> 19  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Synthetic oligonucleotide

<400> 19  
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<210> 20  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Synthetic oligonucleotide

<400> 20  
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<210> 21  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Synthetic oligonucleotide

<400> 21  
 gttttcccca tggcagaga 19

<210> 22  
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<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic oligonucleotide

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ctttgatgga tcaagtaaca cagaaacact aac

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<210> 24

<211> 23

<212> DNA

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<400> 24

gactccatgg caatcccagt gcg

23